Practical Experience with the Use of Halides for Phasing Macromolecular Structures: A Powerful Tool for Structural Genomics

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The crystal structure of pepstatin-insensitive carboxyl proteinase (PCP) from *Pseudomonas* sp.101, an enzyme with no overall sequence similarity to any other proteinases of known structure, was solved by using crystals soaked in sodium bromide solution and then cryocooled. A data set collected at the bromine peak absorption wavelength was sufficient for calculation of an excellent map, and the entire process of phasing and tracing the maps required almost no direct human intervention. The process of structure solution using single-wavelength data was compared with 3-λ multiwavelength anomalous diffraction (MAD); although the latter resulted in slightly better maps, the use of this much more labor-intensive approach did not significantly improve the ability to solve the structure. The successful phasing approaches are compared with several less successful attempts utilizing other crystal forms of the enzyme, and the practical aspects of the use of bromine as a heavy atom derivative are discussed. In conclusion, the use of halides with single-wavelength diffraction data fulfills the requirements of being a first-choice method of high-throughput structure solution for the emerging field of structural genomics.